

| | | | | | | |
|------------|-------|--|------|-----|-----|-----|
| CC | CKR2B | MLSTSRSRIRNTNES CEEV --TTPFDYDY--GAPCHRFDVKOIGAQQLPPLYSLVTFIFGVGNMIVYLINCKKLKCLTDYKLNLAISDLPLITLPLWAH-SAAAEWVY | 20 | 40 | 60 | 80 |
| CC | CKR5 | NDYQV-SSPIYDNYTTSÉPCOKINVQIAAULPPLYSLVTFIFGVGNRVTILINCKRLBMTDYLNLAKASDLPFLTYFWAYTLAAC-WDT | | | | |
| CC | CKR1 | NET TIEDYDTT --EFDYGDAFPCQKVNEJAFCAQQLPPLYSLVTFIFGVGNRVTILINCKRLBMTDYLNLAKASDLPFLTYFWAYTLAAC-WDT | | | | |
| III | | | | | | |
| | | GUANCKLPTGLYHIGTYGIPPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | 100 | 120 | 140 | 160 |
| | | GNTMCQLLTGUYFIGPFGSIFPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| | | GDANCKLISGFYTGLYSEITFILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| IV | | | | | | |
| | | GUANCKLPTGLYHIGTYGIPPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | 200 | 220 | | |
| | | GNTMCQLLTGUYFIGPFGSIFPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| | | GDANCKLISGFYTGLYSEITFILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| V | | | | | | |
| | | GUANCKLPTGLYHIGTYGIPPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | 240 | 260 | 280 | 300 |
| | | GNTMCQLLTGUYFIGPFGSIFPIILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| | | GDANCKLISGFYTGLYSEITFILLTIDRYLAIVHAVALKARTTVFGVNTSVITLWAVTAASPGIITTKCQBDSSVVCGPYPPRG---YNNFHHTIKRNILGLVLPLLLHIVTCYSGILKTLLRCR | | | | |
| VI | | | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | 320. | 340 | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| VII | | | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | 360 | 380 | 400 | 420 |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| IX | | | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | 440. | 460 | 480 | 500 |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |
| | | NEKKERHARVIFTINTVTPFLWTPNIVLNTTQBFYGLSNCESTSQLDQATOVTETLGMTHECCINPIIXYAFVGKEFRAYLSVTFRKQCPVFTRETVDGVTSTNTPSTGEQEVSAGL | | | | |

FIGURE 1A

SEQ ID NO: 1

1 11
TAT CGG TCG ACC CCC ATT ATG GAT GAA TGG CAA GAA ACT CTC CCG CCC TGG AAC AAC AGC
asp pro ser thr ala 11 met asp gly trp gln glu thr leu phe gly trp asn lys met
61 / 21 91 / 31
GAT TAT CAA GTC TCA ACT CCA ATC TAT GAC ATC AAT TAT TAT ACA TCC GAG CCC TGC CAA
asp tyr gln val ser ser pro ile tyr asp ile ASN tyr tyr ser glu pro cys aln
121 / 41 131 / 51
AAA ATC AAT GTC AAC CAA ATC GCA GGC CCC CTC CTG CCT CGG CTC TAC TCA CTC CTC TTC
lys ile ASN val lys gln ile ala ala arg 141 leu pro pro ile tyr ser leu val phe
181 / 61 211 / 71
ATC TTT GGT TTT GTC GCC AAC ATG CTC GTC ATC CTC ATA AAC TCC AAA AGG CTC
ile phe gly phe val gly ASN met leu val ile 141 leu ile ASN cys lys arg leu
241 / 81 271 / 91
AAG AGG ATG ACT GAC ATC TAC CTC CTC AAC CTG GCT ATC TCT GAC CTG TTT TTC CTT CTT
lys ser met thr asp ile tyr 141 leu ASN ala ASN ser asp leu phe leu val leu
301 / 101 331 / 111
ACT GTC CCC TTT TCC CCT CAC TAC TTG GCU GCC GAG TGG GAC TTT GAA RAT ACA ATG TGT
thr val pro phe trp ala his tvt leu ala ala gln trp asp phe gly ASN thr met cys
361 / 121 391 / 131
CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC TCT CGA ATC TTC TTC ATC ATC CTC
gln leu leu thr gly 141 phe phe ASN ser gly ile phe phe ile ile leu
421 / 141 451 / 151
CTG ACA ATC CAT ACC TAC CTC CCT GTC CTC CAT CCT CTG TTT CCT TTA AAA GCC AGG AGG
leu thr 141 ASP ARG TYR leu ala val val HIS ala val phe ala 141 lys ala ARG THR
481 / 161 511 / 171
GTC ATC TTT CCC CTC CTC ACA ACT CTC ATC ACT TGG CTC GTC CCT GTC TTT CGG TTT CTC
val thr phe gly val val thr ser val ile ASN val val ASN val phe ala ser leu
541 / 181 571 / 191
CCA CGA ATC ATC TTT ACT ACA TCT CAA AAA GAA GGT CTT CAT TAC ACC TGC ACC TCT CAT
pro gly ile ASN thr ASN ser Gln lys Glu Gly leu HIS TYR THR CYS ser ASN HIS
601 / 201 631 / 211
TTT CCA TAC AGT CAG TAT CAA TTC TGG AAC AAT TTC CAG ACA TTA AAC ATA GTC ATC TTG
phe PRO TYR ser Gln TYR ASN phe ASN phe ASN THR leu Lys ile Val ASN Thr leu
661 / 221 691 / 231
GGG CTC GTC CTC CGG CTC CTT GTC ATC GTC TAC TGG CGA ATC CTA AAA ACT CTC
gly leu val 141 pro leu leu val met val ile CYS TYR ser GLY ASN leu Lys THR leu
721 / 241 751 / 251
CTT CGG TGT CCA ATC GAG AAC AAC AGC CAC AGG CCT GTC AGG CTT ATC TTC ACC ATC ATG
leu ARG CYS ARG ASN Glu Lys Iys Arg HIS ASN ala Val ARG leu ASN ASN THR PHE ASN
781 / 261 811 / 271
ATT GTT TAT TTT CTC TTC TGG CCT CCC TAC AAC ATT GTC CTT CTC CTC AAC AAC TTC CAG
ile Val TYR phe leu phe trp ASN PRO TYR ASN ile Val 141 leu ASN THR phe ASN
841 / 281 871 / 291
CAA TCC TTT GGC CTC AAT RAT TCC AGT AGC TCT AAC AGC TTS GAC CAA GGT ATC CAG GTC
glu phe phe gly leu ASN ASN CYS ser ser ASN
901 / 101 931 / 111
ACA GAG ACT CTT GGC ATC ACG CAC TCC TWC ATC AAC CCC ATC ATC TAT CCC TTT GTC CGG
THR Glu THR leu GLY MET THR HIS CYS CYS ASN ASN PRO ASN ASN ASN ASN ASN ASN ASN ASN
961 / 121 991 / 131
GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC CAA AAA CAC ATT CCC AAA CGC TTC TCC
glu lys phe ASN ASN TYR leu leu Val phe ASN
1021 / 141 1051 / 151
AAA TGC TGT TCT ATT TTC CAG CAA GAG CCT CCC GAG CGG CGA GCA AGC TCA GTT TAC ACC CGA
lys CYS CYS ser ASN phe ASN
1081 / 161 1111 / 171
TCC ACT CGG GAG CAG GAA ATA TCT GTC CCC TTG TCA TAC GCA CTC AAC TGG CCT CCT GAC
SER THR GLY GLU GLU ASN SER VAL GLY LEU ASN HIS GLY LEU LYS TRP ASN GLY ASN
1141 / 181 1171 / 191
CCA CTC AGA GTC GTC CAC ATG GCT TAG TTT TCA TAC ACA CCC TGG CCT CGG CCT CGG GTC
PRO VAL ARG VAL VAL HIS ASN
1201 / 201 1231 / 211
CCA GAG GTC TTT TTT AAA AGG AAC TTA CTG TTA TAG AGC GTC TAA CAT TCA TCC ATG
GLY GLU VAL PHE PHE LYS ARG LYS 141 LEU LEU ASN ARG VAL OCT ASN SER SER

FIGURE 1B

Figure 1C

SEQ ID NO:3

1 aagaaactct cccgggtgg aacaagatgg attatcaagt gtcaagtcca atctatgaca
61 tcaattatta tacatcgtag ccctgcggaaa aaatcaatgt gaagcaaatac gcagcccccc
121 tcctgcctcc gctctactca ctgggttca ttggggta tgggggcaac atgtggca
181 tcctcatccct gataaaactgc aaaaggctga agagcatgac tgacatctac ctgctcaacc
241 tggccatctc tgacctgtttt tccttcata ctgtccctt ctgggctcac tatgtgcggcc
301 cccagtggga ctggaaat acaatgtgc aactcttgac agggcttat ttataggt
361 tcttcctcgg aatcttcattc atcatccctcc tgacaatcga taggtacccg gctgtcgcc
421 atgcgtgttt tgctttaaaaa gccaggacgg tcacccgttgg ggtgggaca agtgtgatca
481 ctgggttgtt ggctgtgtttt ggctcttc caggaatcat ctgttaccaga tctcaaaaag
541 aaggcttcata acatccctgc agtcttcattt tcctacatcag tcaatgttca tctggaaaga
601 atttcagac attaaagata gtcatctgg ggctggctt gcccgtgtt gtcatggca
661 tctgtactc gggaaatcata aaaactctgc ttccgggtcg aaatgagaag aagaggcaca
721 gggctgttag gctttatcttc accatcatga ttgtttttt tcttttttgc tcccttata
781 acattgtcct tcttcataac accttcagg aattcttgg cctgaataat tgcagtagct
841 ctaacaggtt ggaccaagct atgcagggtga cagagactct tggtatgacg cactgctgca
901 tcaacccat catctatgcc ttgtcgaaaaa agaaggctcag aaactacccctt ttagtctt
961 tccaaaagca cattggccaaa cgcttcgtca aatgcgttc tattttccag caagaggctc
1021 ccgagcggc aagctcagg tacacccat ccactggggaa gcaaggaaata tctgtgggtt
1081 tgtgacacgg actcaagtgg gctgggtgacc cagtcagatgtt gtcacatgtt gcttagttt
1141 catacacacgg ctgggctgggg ggtgggggtgg gagaggtctt ttttttttttttttttttt
1201 tatagagggtt ctaagattca tccat

SEQ ID NO:4

MDYQVSSPIYDINYYTSEPCQKINVKQIAARLLPPLYSLVFIFGFVGNMLVILILINCKRL
KSMTDIYLLNL AISDLFFLLTVPFWAHYAAAQWDFGNTMCQ
LLTGLYFIGFFSGIFFIILLTIDRYLAVHAVFALKARTVTFGVVTSVITWWVAVFAS
LPGIIFTRSQKEGLHYTCSSHFPYSQYQFWKNFQLKIVILGLVLPLLVMVICYSGL
KTLLRCRNEKKRRAVRLLIFTIMIVYFLFWAPYNIVLLNTFQEFFGLNNCSSNRLD
QAMQVTETLGMTHCCINPIIYAFVGEKFRNYLLVFFQKHIAKRFCKCCSIFQQEAPER
ASSVYTRSTGEQEISVGL

Effects of CCR5 Synthetic Peptides on HIV Env-Mediated Fusion

FIGURE 2

